

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME : Genset SA
- (B) STREET : 24, RUE ROYALE
- (C) CITY : PARIS
- (E) COUNTRY : France
- (F) POSTAL CODE (ZIP) : 75008

(ii) TITLE OF INVENTION: Lipoprotein-regulating medicaments

(iii) NUMBER OF SEQUENCES: 14

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy Disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: Win95
- (D) SOFTWARE: Word

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 amino acids
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

PheX(5) [AsnAsp]X(4) [PheTyrTrpLeu]X(6) PheX(5)GlyXTyrXPhe X [PheTyr]

31

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

[SerThr]XPhe [SerTh] Gly [PheTyr]Leu [LeuVal] [PheTyr]

9

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Leu Arg Cys Val Pro Arg Val Leu Gly Ser Ser Val Ala Gly Tyr  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Cys Tyr Ile Thr Phe Leu Glu Asp Leu Lys Ser Phe Val Lys Ser Gln  
1 5 10 15

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: Identical to 58 .. 73 in ref genbank :U49915  
(B) LOCATION: 12..27

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

CTACATGGAT CCAGTCATGC CGAAGAT

27

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 28 base pairs  
(B) TYPE: NUCLEIC ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: DNA

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: Identical to 745 .. 762 in ref genbank :U49915  
(B) LOCATION: complement 11..28

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CGACAACTCG AGTCAGTTGG TATCATGG

28

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 129 amino acids  
(B) TYPE: AMINO ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: fragment 117-245 of ref swissprot :P02745

(ix) FEATURE: (A) NAME/KEY: Consensus box corresponding to  
SEQ ID 1 (B) LOCATION: 17-47

(ix) FEATURE:

(A) NAME/KEY: Consensus box corresponding to SEQ ID 2  
(B) LOCATION: 118-126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Phe Ser Ala Ile Arg Arg Asn Pro Pro Met Gly Gly Asn Val Val Ile  
 1 5 10 15  
 Phe Asp Thr Val Ile Thr Asn Gln Glu Glu Pro Tyr Gln Asn His Ser  
 20 25 30  
 Gly Arg Phe Val Cys Thr Val Pro Gly Tyr Tyr Phe Thr Phe Gln  
 35 40 45  
 Val Leu Ser Gln Trp Glu Ile Cys Leu Ser Ile Val Ser Ser Ser Arg  
 50 55 60  
 Gly Gln Val Arg Arg Ser Leu Gly Phe Cys Asp Thr Thr Asn Lys Gly  
 65 70 75 80  
 Leu Phe Gln Val Val Ser Gly Gly Met Val Leu Gln Leu Gln Gln Gly  
 85 90 95  
 Asp Gln Val Trp Val Glu Lys Asp Pro Lys Lys Gly His Ile Tyr Gln  
 100 105 110  
 Gly Ser Glu Ala Asp Ser Val Phe Ser Gly Phe Leu Ile Phe Pro Ser  
 115 120 125  
 Ala

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 130 amino acids
  - (B) TYPE: AMINO ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PEPTIDE
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
  - (A) NAME/KEY: fragment 122-251 of ref swissprot :P02745
- (ix) FEATURE:
  - (A) NAME/KEY: Consensus box corresponding to SEQ ID 1
  - (B) LOCATION: 19-49
- (ix) FEATURE:
  - (A) NAME/KEY: Consensus box corresponding to SEQ ID 2
  - (B) LOCATION: 117-125
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Phe Ser Ala Thr Arg Thr Ile Asn Val Pro Leu Arg Arg Asp Gln Thr  
 1 5 10 15

Ile Arg Phe Asp His Val Ile Thr Asn Met Asn Asn Asn Tyr Glu Pro  
20 25 30

Arg Ser Gly Lys Phe Thr Cys Lys Val Pro Gly Leu Tyr Tyr Phe Thr  
35 40 45

Tyr His Ala Ser Ser Arg Gly Asn Leu Cys Val Asn Leu Met Arg Gly  
50 55 60

Arg Glu Arg Ala Gln Lys Val Val Thr Phe Cys Asp Tyr Ala Tyr Asn  
65 70 75 80

Thr Phe Gln Val Thr Thr Gly Gly Met Val Leu Lys Leu Glu Gln Gly  
85 90 95

Glu Asn Val Phe Leu Gln Ala Thr Asp Lys Asn Ser Leu Leu Gly Met  
100 105 110

Glu Gly Ala Asn Ser Ile Phe Ser Gly Phe Leu Leu Phe Pro Asp Met  
115 120 125

Glu Ala  
130

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 124 amino acids
  - (B) TYPE: AMINO ACID
  - (C) STRANDEDNESS: SINGLE
  - (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: PEPTIDE
- (vi) ORIGINAL SOURCE:
  - (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
  - (A) NAME/KEY: fragment 121-244 of ref swissprot :P02745
- (ix) FEATURE:
  - (A) NAME/KEY: Consensus box corresponding to SEQ ID 1
  - (B) LOCATION: 19-49
- (ix) FEATURE:
  - (A) NAME/KEY: Consensus box corresponding to SEQ ID 2
  - (B) LOCATION: 114-122
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Phe Thr Val Thr Arg Gln Thr His Gln Pro Pro Ala Pro Asn Ser Leu  
1 5 10 15

Ile Arg Phe Asn Ala Val Leu Thr Asn Pro Gln Gly Asp Tyr Asp Thr  
20 25 30

Ser Thr Gly Lys Phe Thr Cys Lys Val Pro Gly Leu Tyr Tyr Phe Val  
 35 40 45  
 Tyr His Ala Ser His Thr Ala Asn Leu Cys Val Leu Leu Tyr Arg Ser  
 50 55 60  
 Gly Val Lys Val Val Thr Phe Cys Gly His Thr Ser Lys Thr Asn Gln  
 65 70 75 80  
 Val Asn Ser Gly Gly Val Leu Leu Arg Leu Gln Val Gly Glu Glu Val  
 85 90 95  
 Trp Leu Ala Val Asn Asp Tyr Tyr Asp Met Val Gly Ile Gln Gly Ser  
 100 105 110  
 Asp Ser Val Phe Ser Gly Phe Leu Leu Phe Pro Asp  
 115 120

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: fragment 64-193 of translation from ref genbank

:M58583

(ix) FEATURE:

- (A) NAME/KEY: Consensus box corresponding to SEQ ID 1
- (B) LOCATION: 23-53

(ix) FEATURE:

- (A) NAME/KEY: Consensus box corresponding to SEQ ID 2
- (B) LOCATION: 120-128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Phe Ser Ala Ile Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn  
 1 5 10 15  
 Arg Thr Met Ile Ile Tyr Phe Asp Gln Val Leu Val Asn Ile Gly Asn  
 20 25 30  
 Asn Phe Asp Ser Glu Arg Ser Thr Phe Ile Ala Pro Arg Lys Gly Ile  
 35 40 45  
 Tyr Ser Phe Asn Phe His Val Val Lys Val Tyr Asn Arg Gln Thr Ile  
 50 55 60

Gln Val Ser Leu Met Leu Asn Gly Trp Pro Val Ile Ser Ala Phe Ala  
65 70 75 80

Gly Asp Gln Asp Val Thr Arg Glu Ala Ala Ser Asn Gly Val Leu Ile  
85 90 95

Gln Met Glu Lys Gly Asp Arg Ala Tyr Leu Lys Leu Glu Arg Gly Asn  
100 105 110

Leu Met Gly Gly Trp Lys Tyr Ser Thr Phe Ser Gly Phe Leu Val Phe  
115 120 125

Pro Leu  
130

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 amino acids  
(B) TYPE: AMINO ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens

(ix) FEATURE:  
(A) NAME/KEY: fragment 115-244 of translation from ref genbank  
:D45371

(ix) FEATURE:  
(A) NAME/KEY: Consensus box corresponding to SEQ ID 1  
(B) LOCATION: 18-48

(ix) FEATURE:  
(A) NAME/KEY: Consensus box corresponding to SEQ ID 2  
(B) LOCATION: 118-126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Phe Ser Val Gly Leu Glu Thr Tyr Val Thr Ile Pro Asn Met Pro Ile  
1 5 10 15

Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp Gly Ser  
20 25 30

Thr Gly Lys Phe His Cys Asn Ile Pro Gly Leu Tyr Tyr Phe Ala Tyr  
35 40 45

His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe Lys Lys  
50 55 60

Asp Lys Ala Met Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Asn Asn Val

65 70 75 80  
Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly Asp Gln  
85 90 95  
Val Trp Leu Gln Val Tyr Gly Glu Gly Arg Asn Gly Leu Tyr Ala  
100 105 110  
Asp Asn Asp Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr His Asp  
115 120 125  
Thr Asn  
130

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 amino acids  
(B) TYPE: AMINO ACID  
(C) STRANDEDNESS: SINGLE  
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Mus musculus*

(ix) FEATURE:  
(A) NAME/KEY: fragment 118-247 of translation from ref genbank  
:U49915

(ix) FEATURE:  
(A) NAME/KEY: Consensus box corresponding to SEQ ID 1  
(B) LOCATION: 18-48

(ix) FEATURE:  
(A) NAME/KEY: Consensus box corresponding to SEQ ID 2  
(B) LOCATION: 118-126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Phe Ser Val Gly Leu Glu Thr Arg Val Thr Val Pro Asn Val Pro Ile  
1 5 10 15

Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp Asn Ser  
20 25 30

Thr Gly Lys Phe Tyr Cys Asn Ile Pro Gly Leu Tyr Tyr Phe Ser Tyr  
35 40 45

His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe Lys Lys  
50 55 60

Asp Lys Ala Val Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Lys Asn Val  
65 70 75 80

Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly Asp Gln  
85 90 95

Val Trp Leu Gln Val Tyr Gly Asp Gly Asp His Asn Gly Leu Tyr Ala  
100 105 110

Asp Asn Val Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Phe His Asp  
115 120 125

Thr Asn  
130

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 130 amino acids
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:  
(A) ORGANISM: *Mus musculus*

(ix) FEATURE:  
      (A) NAME/KEY: fragment 118-267 of translation from ref genbank

(ix) FEATURE:  
      (A) NAME/KEY: Consensus box corresponding to SEQ ID 1  
      (B) LOCATION: 18-48

(ix) FEATURE:  
      (A) NAME/KEY: Consensus box corresponding to SEQ ID 2  
      (B) POSITION: 1

## 4.1. SEQUENCE 8: THE CHURCH

Phe Ser Val Gly Leu Glu Thr Arg Val Thr Val Pro Asn Val Pro Ile  
1 5 10 15

Arg Phe Thr Lys Ile Phe Tyr Asn Gln Gln Asn His Tyr Asp Gly Ser  
 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47

Thr Gly Lys Phe Tyr Cys Asn Ile Pro Gly Leu Tyr Tyr Phe Ser Tyr  
25 10

His Ile Thr Val Tyr Met Lys Asp Val Lys Val Ser Leu Phe Lys Lys  
52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70

Asp Lys Ala Val Leu Phe Thr Tyr Asp Gln Tyr Gln Glu Lys Asn Val  
65 70 75 80 85 90 95 100

Asp Gln Ala Ser Gly Ser Val Leu Leu His Leu Glu Val Gly Asp Gln  
85 86

Val Trp Leu Gln Val Tyr Gly Asp Gly Asp His Asn Gly Leu Tyr Ala  
100 105 110

Asp Asn Val Asn Asp Ser Thr Phe Thr Gly Phe Leu Leu Tyr His Asp  
115 120 125

Thr Asn  
130

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 126 amino acids
- (B) TYPE: AMINO ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: PEPTIDE

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: fragment 1161-1286 of translation from ref  
genbank :U27109

(ix) FEATURE:

- (A) NAME/KEY: Consensus box corresponding to SEQ ID 1
- (B) LOCATION: 17-47

(ix) FEATURE:

- (A) NAME/KEY: Consensus box corresponding to SEQ ID 2
- (B) LOCATION: 116-124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Phe Phe Ala Ser His Thr Tyr Gly Met Thr Ile Pro Gly Pro Ile Leu  
1 5 10 15

Phe Asn Asn Leu Asp Val Asn Tyr Gly Ala Ser Tyr Thr Pro Arg Thr  
20 25 30

Gly Lys Phe Arg Ile Pro Tyr Leu Gly Val Tyr Val Phe Lys Tyr Thr  
35 40 45

Ile Glu Ser Phe Ser Ala His Ile Ser Gly Phe Leu Val Val Asp Gly  
50 55 60

Ile Asp Lys Leu Ala Phe Glu Ser Glu Asn Ile Asn Ser Glu Ile His  
65 70 75 80

Cys Asp Arg Val Leu Thr Gly Asp Ala Leu Leu Glu Leu Asn Tyr Gly  
85 90 95

Gln Glu Val Trp Leu Arg Leu Ala Lys Gly Thr Ile Pro Ala Lys Phe

100

105

110

Pro Pro Val Thr Thr Phe Ser Gly Tyr Leu Leu Tyr Arg Thr  
115 120 125